

Classification of pulmonary neuroendocrine tumors: new insights

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Abstract: Neuroendocrine tumors of the lung (Lu-NETs) embrace a heterogeneous family of neoplasms classified into four histological variants, namely typical carcinoid (TC), atypical carcinoid (AC), large cell neuroendocrine carcinoma (LCNEC) and small cell lung carcinoma (SCLC). Defining criteria on resection specimens include mitotic count in 2 mm² and the presence or absence of necrosis, alongside a constellation of cytological and histological traits including cell size and shape, nuclear features and overall architecture. Clinically, TC are low-grade malignant tumors, AC intermediate-grade malignant tumors and SCLC/LCNEC high-grade malignant full-blown carcinomas with no significant differences in survival between them. Homologous tumors arise in the thymus that occasionally have some difficulties in differentiating from the lung counterparts when presented with large unresectable or metastatic lesions. Immunohistochemistry (IHC) helps refine NE diagnosis at various anatomical sites, particularly on small-sized tissue material, in which only TC and small cell carcinoma categories can be recognized easily on hematoxylin & eosin stain, while AC and LCNEC can only be suggested on such material. The Ki-67 labeling index effectively separates carcinoids from small cell carcinoma and may prove useful for the clinical management of a metastatic disease to help the therapeutic decision-making process. Although carcinoids and high-grade neuroendocrine carcinomas in the lung and elsewhere make up separate tumor categories on molecular grounds, emerging data supports the concept of secondary high-grade NETs arising in the preexisting carcinoids, whose clinical and biological relevance will have to be placed into the proper context for the optimal management of these patients. In this review, we will discuss the selected, recent literature with a focus on current issues regarding Lu-NET nosology, i.e., classification, derivation and tumor evolution.

Keywords: Immunohistochemistry (IHC); classification; lung; neuroendocrine; tumor

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Introduction

Neuroendocrine tumors of the lung (Lu-NETs) make up a heterogeneous family of neoplasms ranging from quite indolent lesions with long-term life expectancy to extremely aggressive tumors with very poor prognosis. The 2015 WHO classification has grouped the four histologic variants of Lu-NETs, namely typical carcinoid (TC), atypical carcinoid (AC), large cell neuroendocrine carcinoma (LCNEC) and small cell lung carcinoma (SCLC), into a unique box of neuroendocrine (NE) cell proliferations to facilitate their taxonomy and improve diagnostic recognition (1,2). Behaviorally, TC are low-grade tumors with good prognosis usually cured by surgery alone, AC intermediate-grade tumors with a more aggressive clinical course benefitting from multimodality therapy, and LCNEC and SCLC high-grade full-blown carcinomas with dismal prognosis usually treated by chemo-radiotherapy (1). Although tumor grading is included into the current classification scheme, as considerable clinical and epidemiologic data have been validating a pathologic four-tier, clinical three-tier spectrum of NE-differentiated tumors (1,3), a grading system independent of histology could prove useful in the setting of a metastatic disease and/or small-sized diagnostic material, where morphology alone could not match adequately with the pathologic and clinical grade to support the best therapy choices (4,5).

Tumors homologous with Lu-NENs arise in the thymus (T-NENs) and gastro-entero-pancreatic tract (GEP-NENs), likely due to their common origin from endoderm-derived precursors/stem cells of the foregut according to specific molecular gene pathway alterations (6-11). Significant differences, however, in the biological characteristics of these tumors make a direct comparison with Lu-NETs clinically unwarranted (12-23). Suffice it to say that a backbone observation regarding NENs is that they behave diversely according to the different anatomical sites (23,24), associated risk factors and underlying molecular mechanisms (24-29). However, differences in cell lineage or the diverse application of defining criteria may cause some inconsistency to arise in the diagnostic, prognostic and predictive interpretation (8-11). This bewildering situation becomes even more challenging and frustrating when dealing with metastatic NENs of unproven or uncertain origin and/or small-sized diagnostic material, where morphology alone may be a major pitfall in the management of tumor patients (5,30-36).

The classification of Lu-NETs is a stepwise process based on a constellation of cytological and histological traits alongside the evaluation of mitotic count and necrosis extent (1,2). At variance with its established role in GEP NENs according to existing guidelines (37,38) and the forthcoming 2017 WHO classification on non-pulmonary neuroendocrine tumors, immunohistochemistry (IHC) for NE markers is not strictly required to render an ultimate diagnosis of Lu-NETs. Nonetheless, it is recommended to confirm their NE nature and, particularly, to separate LCNEC from other histologic mimickers, such as large cell carcinoma with NE morphology (LCC-NEM) and basaloid carcinoma, or to identify combined variants with non-small cell carcinoma (NSCC) components (1,2).

Lung TC and AC as a whole are pragmatically equated to well-differentiated neoplasms in opposition to SCLC and LCNEC, which are collectively poorly differentiated tumors closest to the NE carcinoma (NEC) category of GEP NENs (3,8-11). This dichotomy of morphologic classification is consistent with the current assertion that TC and AC in the lung are molecularly distinct from SCLC and LCNEC (1,2,39-43). Major differences in the somatic mutation rate and engagement of diverse gene pathway alterations have been observed in these two main groupings of Lu-NETs (31,42-52); while there is some inter-tumor heterogeneity of molecular events within a category, particularly AC and LCNEC (39,40,53-55). These observations support the view that different patient subsets exist within each variant of Lu-NETs as defined upon histology, with some degrees of overlap among the categories (25,27), suggesting some commonality in their origin, developmental mechanisms, prognosis or treatment options (5,8,9,53-57).

Browsing the recent literature, this review is focused on current Lu-NETs nosology, immunophenotyping, proliferation indices and molecular alterations, trying to place into context all current information for the best management of the patients.

Diagnosis and classification of pulmonary neuroendocrine tumors

TC and AC in the lung retain morphologic criteria of well-differentiated NETs (1,3,58). They are close to the normal NE elements present in the respiratory mucosa, hyperplastic NE cells as seen in chronic inflammation and the diffuse idiopathic pulmonary NE cell hyperplasia (DIPNECH), a pre-invasive lesion with a potential

towards the development of carcinoids (1,59-61). Defining criteria of these tumors include organoid growth patterns (rosettes, trabeculae, ribbons, festoons, lobular nests, palisading), absent to focal punctate necrosis (not just apoptotic bodies), up to 10 mitoses per 2 mm² and a consistent labeling for pan-NE IHC markers, sometimes less intense and uneven in AC (1,3,58,62,63). On the contrary, SCLC and LCNEC are clustered into poorly differentiated tumors showing trabecular to solid to diffuse growth patterns, extensive/geographic necrosis, mitotic count higher than 10 mitoses per 2 mm² with no theoretical upper limit and uneven cell decoration for pan-NE markers, especially those based on dense-core granules (1,3,62-65). Tumor architecture and cytological details serve further to separate LCNEC from SCLC, even though inter-observer reproducibility remains disappointingly low (66-70). LCNEC is a tumor category defined upon pan-NE IHC markers to exclude histological mimics such as LCC-NEM and basaloid carcinoma, or identify non-NE components in combined variants (1,71). The diagnosis of SCLC in turn relies primarily upon morphology in both the lung and elsewhere, although IHC has been recommended to either reduce the rate of misdiagnosis in challenging cases for technical reasons or to increase the diagnostic confidence of pathologists for complex differential diagnoses (65).

In surgical as well as in biopsy/cytology specimens, general markers of NE differentiation provide a reliable profile for all histologic variants of Lu-NETs, while single hormones are less useful even in the metastatic setting or when facing with unknown origin lesions because of the lack of specific substances produced in the lower respiratory tract (72). Current guidelines and longstanding experience recommend using a couple of well-established pan-NE markers to cross the entire spectrum of Lu-NETs (1-3,65,73). Among plentiful pan-NE markers, the most currently used are cytoplasm-based molecules contained in dense core granules, such as chromogranin A, whose presence closely parallels the biogenesis of secretory granules and hence cell differentiation (74), or small clear synaptic vesicles, such as synaptophysin, which regulates the kinetics of synaptic vesicle endocytosis (75) and whose expression is still retained in high-grade Lu-NETs (1-3,65,73). As poorly differentiated Lu-NET down-regulate chromogranin A, its expression should be evaluated at high-power magnification to appreciate even faint granular signals in scattered tumor cells (1). Embryonic nuclear determinants of NE differentiation in the lung,

such as human achaete-scute homolog 1 (hASH1), are usually lost or poorly expressed in carcinoids but retained by high-grade tumors, especially SCLC (76,77), whereas membrane-based NCAM/CD56 is sensitive but less specific for NE differentiation (1,78). The latter is expressed in all Lu-NETs, especially SCLC (40,77-79), but can turn out positive also in conventional NSCC (80), various sarcomas (81,82) and malignant mesothelioma (83). High molecular weight keratins (CK), such as those recognized by the clone 34βE12 (CK1, CK5, CK10 and CK14), are consistently negative in Lu-NETs (84). The squamous differentiation determinant DeltaNp63/p40 is unreactive in all variants of Lu-NETs (85), although its expression is found rarely in some LCNEC exhibiting morphology and molecular alterations more akin to SCLC (40). These tumors with focal (≤10% tumor cells) positivity for DeltaNp63/p40 but no overt squamous differentiation harbor a high prevalence of KEAP1-NFE2L2 alterations, suggesting that they are somewhat linked to squamous cell carcinoma rather than conventional SCLC (40).

Another nuclear determinant of NE differentiation, i.e., insulinoma-associated protein 1 (INSM1), has recently been proposed to stain consistently all variants of Lu-NET regardless of histology, but not conventional adenocarcinoma or squamous cell carcinoma (86,87). This marker is potentially expected to work better than the usual pan-NE antigens because of its wide range of expression across the entire spectrum of Lu-NETs, and could become a reference molecule for NE differentiation in the near future. In general, nuclear markers are less likely affected by cellular damage, thus remain intact on small-sized and/or crushed tissue samples, while organelle- or membrane-associated markers may suffer from non-specific staining due to extracellular extravasation or may not consistently reflect their own locations in the cytoplasm (88). Albeit rare in the lung but less in the mediastinum, nuclear in testis (NUT) midline carcinoma (NMC) (88,89), Ewing sarcoma family (ESF) (90) and desmoplastic small round cell tumor (DSRCT) (91) should also be accounted for in the differential diagnosis of high-grade NETs especially when facing with large unresectable or metastatic lesions, due to close similarities in histologic appearance and striking overlap of IHC markers with more conventional thoracic NETs. In this regard, an appropriate IHC for NUT protein in NMC and specific molecular investigation for diagnostic translocations in ESF and DSRCT allow the correct diagnosis to be rendered in most cases with high rate of confidence.

Identifying the origin of neuroendocrine tumors

The identification of thoracic NEN origin plays an important role in adopting the most appropriate terminology, correctly classifying metastatic tumors and offering the best therapeutic options (1,2,92), given that lung and thymus NETs differ in tumor presentation (7,12,14), associated endocrine syndromes (12,13,16,18,19,21,93,94), underlying risk factors (1,15) and molecular alterations (1,95). The differentiation of Lu-NETs from T-NETs proves to be particularly challenging in the setting of low-to intermediate-grade tumors displaying large unresectable or metastatic lesions at the time of diagnosis (96). Whether IHC is able to play some role in this task is outlined below.

Thyroid transcription factor-1 (TTF-1) is a useful marker of pulmonary lineage only when positive in the group of well-differentiated NETs. Of note, only a minority of well-differentiated Lu-NETs, especially those composed of spindle cells arising from peripheral bronchioles, are TTF-1 positive (1,97-102), so as some of DIPNECH or NE cell hyperplasia of the lung (103). The main limitation to the use of this marker in high-grade NECs as a descriptor of lung origin is that most of them demonstrate a diffuse reactivity regardless of their pulmonary or extra-pulmonary derivation (1,102,104). Moreover, some T-NETs (93) may be reactive for TTF-1 even when using the most specific clone 8G7G3/1, thus TTF-1 may not be a reliable maker to confirm the pulmonary origin in thoracic NETs. Many other nuclear transcription factors, which are frequently used to differentiate well differentiated NETs in diverse organs, namely Islet-1 (103,105,106), PAX-8 (101,105) and CDX2 (106), can be aberrantly and illegitimately expressed in high-grade NETs regardless of their anatomical locations (31,107). Similarly, CD117 does not separate reliably lung from thymic NETs because is often expressed in both anatomical compartments, especially less differentiated lesions (1,108,109) as well as conventional NSCC (110) and thymic carcinoma (1,92). Conversely, CD5 expression is exceedingly rare in NETs of either anatomical site (23), while CD5 reacts with about a half of thymic squamous cell carcinomas (1,92,111) and a non-negligible fraction of NSCLC (112). Potential confounding factor is represented by combined variants of NETs not only at the level of the IHC characterization (due to co-expression of unexpected profiles and lack of protein expression characteristic of either tumor type), but also at the molecular level (113). It has recently been noted that

mixed NE/non-NE carcinomas are molecularly different from their pure NE and non-NE counterparts in the lung and a variety of extra-pulmonary sites when analyzed for cDNA quantification of ribonucleotide reductase, large subunit 1, excision repair cross-complementation group 1 and thymidylate synthase (114). In this setting of a predominant non-NE component, the administration of adjuvant therapy in addition to surgery and a high thymidylate synthase expression in non-NET components were significantly associated with a lower risk of patient death, thereby improving the clinical strategies for the treatment of these rare and underestimated tumors (114).

The role of IHC becomes particularly relevant in the scenario of small biopsy or cytology samples, where it is clinically warranted to separate NE from other non-NE tumors or unrelated malignancies mimicking NETs in either the lung or thymus. In a recent international study carried out on biopsy samples, the rate of agreement on SCLC diagnosis was increased from 64.7% obtained by the solely morphology to 77.5% with a judicious use of a variety of IHC markers, such as cytokeratin cocktail, pan-NE markers, TTF1, p16 (expressed by high-grade NETs, especially SCLC), retinoblastoma protein and Ki-67 antigen, with Cohen's kappa coefficient scores on IHC being 0.60 and 0.64 in resected specimens and biopsy samples, respectively (65). While the differentiation of SCLC from other unrelated mimics (undifferentiated carcinomas, small cell sarcomas or lymphomas) requires further IHC markers and molecular assays, the single most reliable marker in NETs to get insights into their clinical behavior remains the Ki-67 antigen (1,30,115). This marker is particularly reliable on small biopsy or cytology samples in the presence of scarce material or crush artifacts (32).

Identifying the clinical aggressiveness of neuroendocrine tumors and the role of Ki-67 antigen

Ki-67 antigen has been extensively evaluated in Lu-NET with several diagnostic, prognostic and grading implications [reviewed in (115)]. Since the Ki-67 antigen identifies proliferating cells spanning from G1 to M phase (116-118), Ki-67 nuclear expression is proportional to the mitotic count, but reveals more proliferating tumor cells than the latter, which remains the backbone of defining criteria in Lu-NETs and T-NETs according to existing guidelines (1). The method to quantify Ki-67 expression and that to count mitoses are different; a percentage of Ki-67

positive cells (labeling index, LI) is usually obtained in hot spot regions with highest staining, while the mitotic count is based on the number of mitotic figures in pre-defined tumor areas of highest activity (high power fields or square millimeters). The difference may account in part for inconsistent results between these proliferation indexes (4). Indeed, once mitoses are expressed as mitotic index rather than mitotic count (119), the correlation rate with Ki-67 LI increases considerably (120,121). Furthermore, another source of inconsistency is the alleged lack of inter-observer reproducibility of Ki-67 LI, which is likely attributed to the differences in regions (randomly selected fields; hot spot areas of highest labeling; entire tumor area) and methods (few hundreds to thousands of tumors cells; eyeball, manual or picture-based count evaluation or automated analysis system adoption) for counting Ki-67 positive tumor cells, once pre-analytical issues (fixation, staining systems, reagents) are equated (8,115,122-124). Another conundrum is the intra-tumor heterogeneous distribution of Ki-67 antigen likely due to the unpredictable occurrence of differentially regulated tumor cell subsets in tumors (115,120), but the consistent assessment of labeling indexes in hot spot regions will lead to more reproducible results (115). This biological phenomenon becomes particularly challenging on biopsy/cytology specimens in comparison with resection specimens (30,33,125) because of unpredictable sampling issues (the so-called tip-of-the-iceberg effect or the part of the whole). Therefore, the reproducibility and clinical usefulness of Ki-67 LI in Lu-NETs have been seriously argued, with alleged superiority of mitotic count, which has remained the only proliferation criterion in tumor classifications over time (1,126,127), with no current diagnostic role for Ki-67 (1). However, reproducibility of results for Ki-67 LI is not worse than any other IHC markers when tested for quantification (128,129) and even mitotic count shows large inter-observer variability in Lu-NETs classification of either carcinoids (130) or high-grade tumors (66-70). The only obvious difference is that mitotic count is traditional, largely known by pathologists everywhere and carried out simultaneously with hematoxylin-eosin diagnosis, whereas Ki-67 antigen evaluation requires additional IHC on new paraffin sections and a numeric quantification. Hopefully, the localization of the same tumor areas as those assessed for mitotic count will make results biologically more reasonable (115). Last but not least, the unavailability of IHC in some pathology laboratories would prefer mitotic count over Ki-67 LI in the daily practice. In any event, Ki-67 LI should not

be used as a surrogate of mitotic count, since it is not a current defining criterion, but rather a complementary tool. In contrast, Ki-67 LI is a backbone of the grading system of GEP tract NENs, once tumors are split into well differentiated and poorly differentiated categories based on morphological grounds (8-11,37,131).

A recent standardization of Ki-67 LI on biopsy samples and the corresponding surgical specimens of Lu-NETs have demonstrated that results were quite superimposable with minimal deviation, even among different observers, provided that precise methodology rules were *a priori* established and used in either type of material (30). In keeping with other comparative studies (33,125), it was important to start identifying hot spot regions in either type of material in order to obtain overlapping results when counting 2,000 cells, 2-mm²-spanning areas or the entire biopsy fragment(s) (30). In this way, it was possible to attribute to unpredictable sampling, tissue sizing, intra-tumor heterogeneous distribution of Ki-67 antigen and inter-observer discordance when Ki-67 LI were discrepant between biopsies and the corresponding resection specimens (30). This study also suggests that different methods for the Ki-67 LI assessment but not an inherent unreliability of the marker as a biological predictor affect its clinical meaning (30). Recent reproducibility studies in Lu-NET have revealed that there is less than 1.5% of variability when evaluating Ki-67 LI, with an out-performance over mitotic count with regard to inter-observer agreement (132,133).

Although Ki-67 LI is not currently accredited with Lu-NET subtyping due to some overlap of cut-off thresholds among biologically adjacent tumors (TC *vs.* AC, AC *vs.* LCNEC, LCNEC *vs.* SCLC), its differential distribution between low- to intermediate-grade and high-grade tumors has made it an irreplaceable discriminator especially on biopsy/cytology samples, and recommended even on surgical specimens (1,32,115). A Ki-67 LI up to 20-25% has the highest specificity and sensitivity for low- to intermediate-grade versus high-grade tumors, whilst other IHC markers or a combination of necrosis and mitotic count have lower specificity and sensitivity (1,30,32,115). Given the reported prognostic role of the Ki-67 LI within the same group, such as TC and/or AC, Ki-67 LI has emerged as a reliable criterion for clinical decision-making (132,134-137), in particular, in the setting of metastatic disease. It is important to note that Ki-67 LI closely reflects tumor biology, while the role of the more fallacious morphology is limited in small-sized and/or crushed diagnostic

materials (138). Such an advantage holds particularly true for AC and LCNEC, the most clinically challenging categories of Lu-NETs likely due to the large range of diagnostic criteria (2–10 mitoses in AC; no upper limit over 10 mitoses alongside a wide spectrum of morphology for LCNEC) (1,40,66,67,69,139). Conversely, diagnostic criteria for TC (virtual absence of mitosis and necrosis) and SCLC (undifferentiated morphology, plentiful mitoses, extensive/geographic necrosis) are consistent with biologically and behaviorally more homogeneous categories that occupy the ends of the Lu-NET spectrum (1,73). Not unexpectedly, Ki-67 is typically 5% or less in TC and usually 80% or more in SCLC (118). Our recent observations showed that AC with Ki-67 LI of 10% or more consisted of tumors with more prominent proliferation activity within the allowed range of mitotic count and necrosis, and are associated with worse prognosis than predicted within the tumor category (140). It has also been noted that LCNEC with molecular alterations akin to NSCLC or AC feature the mean Ki-67 LI lower than that of LCNEC with molecular alterations similar to SCLC (i.e., SCLC-like LCNEC), which in turn feature cytomorphology in the SCLC spectrum (40). Other studies have revealed that AC behaviorally can overlap with either TC, SCLC or LCNEC when using Ki-67 LI thresholds specifically designed for the lung (4).

As necrosis and mitoses are unreliable criteria on biopsy samples (1,3,30,58), the differentiation of TC from AC or the diagnosis of LCNEC is usually not permissive on the morphologic basis alone or can only be suggested in these samples (1,141). In Lu-NETs, the main clinical question concerns the need of the patient risk stratification on the basis of tumor aggressiveness, especially in the setting of metastatic disease where the morphology on small-sized diagnostic materials could be misleading (5,138). Therefore, together with the overall clinical profiles (radiology and nuclear medicine imaging, tumor burden, symptoms and individual risk for evolving disease) Ki-67 LI could potentially be a decisional factor to stratify patients into more defined clinical categories for precision medicine (5).

Accordingly, metastatic Lu-NETs can be stratified into four main clinical groups by integrating Ki-67 LI and traditional histology (5).

- (I) The first group consist of completely indolent tumors showing Ki-67 LI of 5% or less, which biologically correspond to either TC or AC with a low mitotic count and could be treated with biological drugs (somatostatin analogues or m-TOR

pathway inhibitors), if any (3,58).

- (II) The second group includes low-to-moderate malignant tumors showing Ki-67 LI up to 20–25%, which biologically correspond to rare TC, most AC and even some LCNEC with a molecular profile similar to that of carcinoids (40). They are probably managed still with biological drugs and/or peptide receptor radionuclide therapy alone (142–144), though no official guidelines yet exist for them (3,58,145,146).
- (III) The third group consists of moderate to higher malignant tumors with Ki-67 LI ranging from 25% to 50–60%, biologically corresponding to more uncommon aggressive AC or LCNEC with a molecular profile similar to that of NSCLC (40). They can be treated with alkylating drugs or others but not with platinum/etoposide-based chemotherapy, such as gemcitabine, paclitaxel or vinorelbine (93,144).
- (IV) The last group is composed of highly malignant tumors with Ki-67 LI ranging from 60% to 100%, biologically corresponding to aggressive SCLC and SCLC-like LCNEC on molecular grounds (41), which should be treated with platinum/etoposide-based chemotherapy (1,144).

Phenotypic/genotypic correlations in Lu-NET showed that a Ki-67 LI over 10% predicts poor prognosis within the AC category outperforming necrosis and mitotic count (140) and that there is a close relationship between proliferation activity and molecular subcategorization of LCNEC (40). For the latter, LCNEC exhibiting a molecular profile similar to that of SCLC had the highest Ki-67 LI (on average 90%), LCNEC harboring NSCLC-like mutations displayed an intermediate value around 60% and those bearing *MEN1* mutations presented with the lowest Ki-67 LI around 35% (40). This peculiar distribution of Ki-67 LI as a function of cell morphology and differentiation levels is similar to what has recently been described in the digestive system under the new classification of GEP NEN tumors, which, along with NET G1 and G2, now includes NET G3, distinct from (poorly differentiated) NEC (144).

Neuroendocrine tumors and molecular alterations

It is widely accepted that Lu-NETs and T-NETs consist of biologically distinct groups but not a continuum of neoplasms with common pathogenesis (1,50,92). In both

anatomical sites, TC/AC on the one hand and LCNEC/SCLC on the other prove separate malignancies when molecularly dissected, with recurrent and non-random alterations of cell cycle checkpoints, chromatin remodeling and recurrent chromosomal alterations (1,50,92,95). Whether genetic traits are better than morphology or IHC markers to distinguish lung from thymus NENs, especially in the setting of large tumors occupying both anatomical regions and metastatic sites, still remains as an unanswered question due to the lack of organ-specific profiles.

TC and AC in the lung (42,44-46,48,50,55,115,147) and the homologous G1-G2 NETs in the GEP tract (24,148) (data thus far are largely unavailable for T-NETs) display lower somatic mutation rates (<1 per million base pairs) compared to the high-grade counterparts likely due to substantial differences in risk factors (1,149-151), gene pathway activations, levels of differentiation and purported cell derivation (42,44-46,48,50,55,115,147). In the lung, defined candidate driver alterations are identifiable in up to 73% of TC and AC (42). Briefly, *RB1* and *TP53* mutations are quite uncommon in TC and AC (152), whereas inactivation of genes affecting histone methylation (*MEN1*) by multiple mechanisms and *SWI/SNF* complex subunit mutations (*ARID1A*, *SMARCB1*, *SMARCA2*, *SMARCA4*) are found in up to one third of cases (42,50-52,55). Additional alterations include mutations of *CBX6*, *EZH2*, *EIF1AX* and E3 ubiquitin ligases (52).

Among high-grade Lu-NETs, LCNEC constitute a heterogeneous family of tumors, with some of them being classified SCLC-like LCNEC accounting for about 40%, NSCLC-like LCNEC (either adenocarcinoma or squamous cell carcinoma) accounting for about 50% and carcinoid-like LCNEC accounting for about 5% on the basis of the different sets of altered genes (40). SCLC-like LCNEC share molecular alterations with SCLC and show *RB1*, *TP53*, *CREBBP*, *EP300* and *MLL* gene mutations (40,42,49) alongside *MYCL1* and *FGFR1* amplifications. NSCLC-like LCNEC exhibit *CDKN2A* deletion, *TTF1* amplifications and *KEAP1* and *STK11* mutations as observed in non-NE tumors (40,42,49) and carcinoid-like LCNEC bear *MEN1* mutations (40,153). SCLC has one of the highest mutation rates in cancers, with inactivating mutations of tumor suppressor genes (*TP53*, *RB1*) and chromatin remodeling genes (*CREBBP*, *EP300*, *MLL*) being more frequently found (42,46,154). Other recurrent gene aberrations include mutations of *PTEN*, *SLIT2*, *COBL*, *EPHA7* and *CDKN2A* genes, along with amplification of *FGFR1*, *MYCL1*, *MYCN*, *MYC*, *SOX2*, *KIAA1432*, *RICTOR*, *JAK2* and *MAD1L1* (42,44,46,48,154-157) and recurrent fusion transcript

RLF-MYCL1 (44,48). Inactivation of *NOTCH* gene upon mutation with simultaneous *ASCL1* and canonical WNT signaling engagement in addition to mutual bi-allelic *RB1* and *TP53* lesions is at the basis of pulmonary and extra-pulmonary small cell carcinoma developing as secondary tumors from preexisting non-NE carcinomas, either spontaneous or induced by therapy (158). Activation of epithelial-mesenchymal transition (EMT) via fascin-induced E-cadherin/ β -catenin system alterations that are responsible for nuclear shuttling of non-mutated β -catenin has been documented in a subset of LCNEC and SCLC (159-161). A further level of complexity in the molecular heterogeneity of Lu-NETs is unraveled by differences in gene expression profiling or diverse expression of functional biomarkers, such as CD44, orthopedia transcription factor, CEACAM and vitamin D-binding protein, which are able to identify patient subsets differentially at risk of progression within each histological variant or tumor group (52,54-56,97,159,162).

Molecular alterations of T-NETs are poorly understood and, in particular, only few next generation sequencing (NGS) studies have been conducted. In these tumors, *MEN1* genotype/phenotype correlation is less significant than in Lu-NETs suggesting the involvement of other genetic factors (15,17,18,20,21). As a matter of fact, about one fourth of T-NETs are *MEN1*-related (20,163), whereas only 1-8% of patients with *MEN1* syndrome develop T-NET during life (15,17,18,163-167). Most of *MEN1*-related T-NETs correspond to carcinoids (163), but even poorly differentiated NE carcinomas (18,168) or purported carcinoids with gross areas of necrosis (15) have been reported. Interestingly, two T-NET cases have recently been reported, in which synchronous or metachronous LCNEC arose within a background of preexisting AC. All tumor components, either AC or LCNEC, presented with *CTNNB1* mutations, which were likely responsible for cyclin D1-*RB1* axis-dependent tumor growth, along with subsequent *TP53* and *JAK3* mutations in one case and EMT activation in the other case leading to de-differentiation and further tumor expansion (23). Chromosomal imbalances, whether loss or gain (95,169,170), and aneuploidy (171) are differentially distributed among the diverse subtypes of T-NETs, with the mean number of chromosomal imbalances being 0.8, 1.1 and 4.7 in TC (31% aberrant cases), AC (44% aberrant cases) and high-grade T-NET (75% aberrant cases), respectively. Gains of 8q24 mapping to *MYC* gene locus was the most frequent alteration and one of the overlapping features between carcinoids and

high-grade T-NENs (95).

Molecular alterations across Lu-NETs, T-NETs or GEP-NENs, yet with different prevalence rates, have recently been documented as mutations, copy number variations and microRNAs (24-27,95,157), thus supporting innovative insights into the developmental mechanisms of these tumors. The existence of combined variants of NETs in several anatomical locations (1,113) and experimental models on the development of secondary SCLC (158) reveal a high plasticity of cancer stem cells through the activation of multiple genetic and epigenetic mechanisms. It could be hypothesized that the occurrence of common genetic events among diversely classified tumors is functional to maintain shared biological, morphological or functional traits and/or that even low grade tumors with well differentiated morphology have a potential to evolve into high-grade NETs (23). Interestingly, Lu-NETs, T-NETs and even GEP NENs with dual components of high- and low-grade tumors in synchronous or metachronous lesions have been identified (23,40,171-178). Further, these tumors share molecular alterations indicative of an origin from common ancestors of lower grade, with additional gene mutations occurring in the high-grade components over time due to temporally delayed clonal evolution of tumor cells. This combination of low-grade and high-grade components has been documented in the thymus (23,173,174) as secondary high-grade NETs, in the lung as NE carcinoma with carcinoid morphology (172) or carcinoids with proliferation rate progression (179), and in the GEP tract as transformed NET, well differentiated NET featuring high-grade components or well differentiated NET with high-grade (G3) progression (180,181). This concept, which would represent a paradigm shift from accepted pathogenesis schemes, has not been included in the current WHO classification of Lu-NETs where carcinoids or NETs are not thought to be usual early forerunners of high-grade lesions (1) and is probably an under-recognized phenomenon in these tumors. The reverse, i.e., down-grading of poorly differentiated NETs, is not supported by the clinical behavior of these tumors (usually more aggressive than lower grade counterparts but less lethal than high-grade tumors) and by the occurrence of the same molecular alterations in both tumor components alongside further aberrations in high-grade elements promoting tumor dedifferentiation, growth and invasion (23). The recently described categories of NET G3 within the GEP tract (113,180) with a preserved well-differentiated NE morphology yet showing a mitotic count above 20 mitoses

per 2 mm² and Ki-67 LI over 20%, the carcinoid-like LCNEC and NE carcinoma with carcinoid morphology (40,172), and synchronous or metachronous thymus LCNEC retaining AC components (23) are instances of secondary high-grade NETs (23) derived from preexisting G1/G2 GEP NETs or lung and thymus TC/AT. *CTNNB1* gene mutations could be one of the molecular alterations underlying the progression in the thymus (23) and GEP tract (26). Similar occurrences, however, have been documented in secondary glioblastoma from long-standing astrocytoma (182,183) or triple negative breast cancer from adenoid cystic carcinoma (184).

The hallmark of such secondary high-grade NETs in the thymus (23) and GEP tract (NV, personal communication) is the presence of concurrent and variably intermingled areas with low or high Ki-67 LI/mitotic counts within a tumor. These evolving tumors would be usually associated with an intermediate clinical course (23,181), unless additional, adverse molecular alterations, such as TP53 inactivation, took place over time (23). An instance of such a tumor arising in the lung is depicted in *Figure 1*, which emphasizes once again the role of Ki-67 LI for diagnosis and biological interpretation. This heterogeneous intra-tumor distribution of Ki67 LI likely results from diversely tuned cell subsets causing hot and cold spot areas to appear within individual tumors. Heterogeneity of Ki-67 LI at metastatic sites and among different metastasis locations as compared with paired primaries was first described in pancreatic NETs (120), but has recently been indicated to occur in stage IV lung carcinoids only in an abstract form (179).

At this point, the clinical and biological questions are related to the frequency of this event and to the level of diagnostic awareness by pathologists. It has been observed that carcinoids and high-grade NE carcinomas in the lung share most of the altered genes, such as mutations, copy number variations and microRNA, even though at different prevalence (24-27,95,157), and that common mutations or chromosomal changes may unexpectedly cluster tumor regardless of histology. This supports a transition from low to high grade in a non-negligible fraction of Lu-NETs (GP, personal experience). To partly explain the apparent contradiction to the widely reported differential distribution of molecular events among diverse NETs in both the lung and elsewhere (1,50,92,95), it should be kept in mind that most of existing molecular data have been derived from the analysis of surgical specimens, where up to one fourth/one third of high-grade NET patients experience longer survival (56).

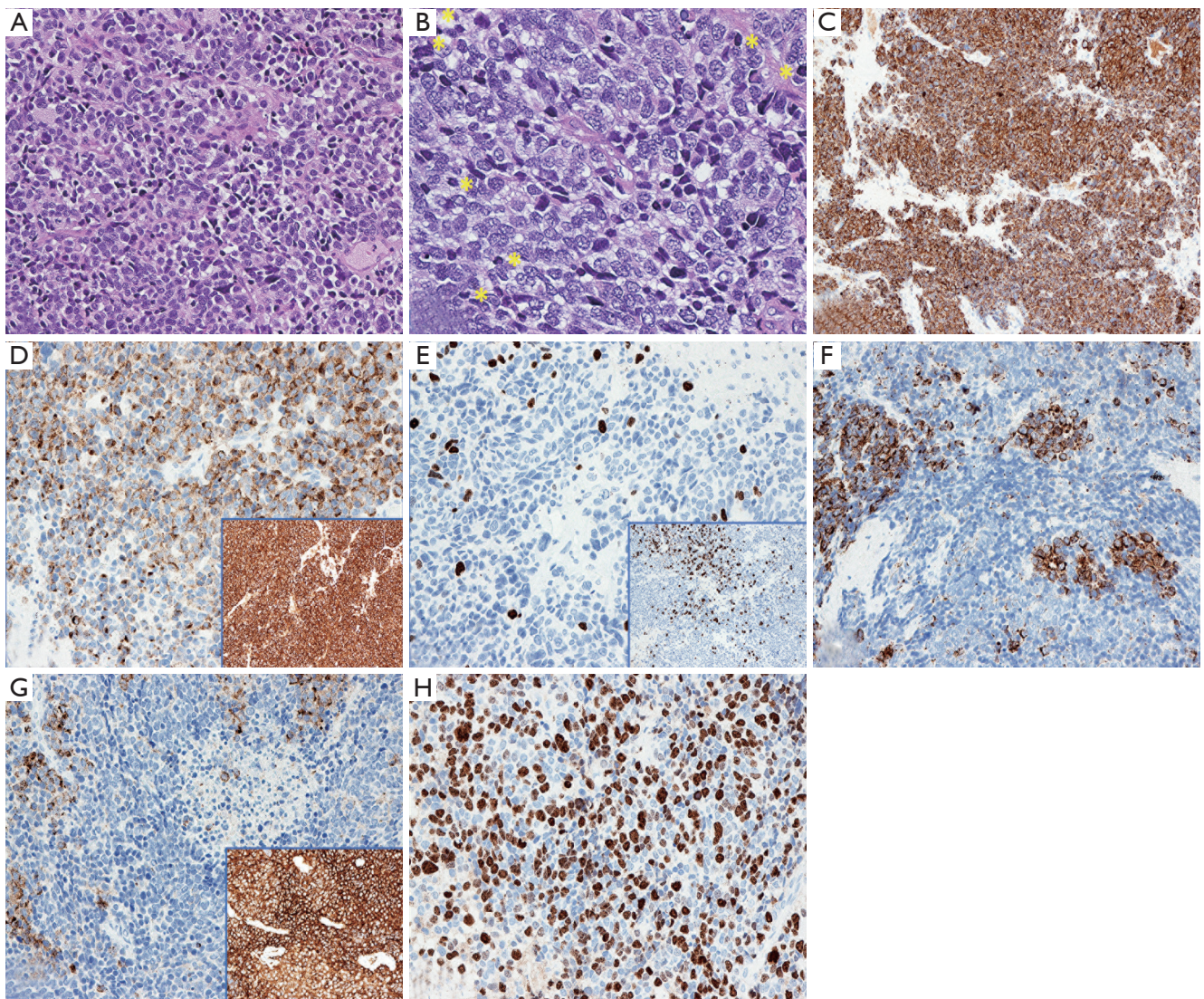


Figure 1 An example of secondary high-grade neuroendocrine tumor of the lung is depicted according to conventional staining and IHC markers (×200). The lower grade component (A) is composed by carcinoid with no obvious mitoses or necrosis spots, whereas the high-grade component (accounting for more than 50% tumor mass) featured small cells with numerous mitotic figures (yellow asterisks) (B). The lower grade component was positive diffusely for cytokeratin cocktail AE1-AE3 (C), chromogranin A (D), and showed low Ki-67 labeling index (about 15%) (E), with transition areas towards higher grade elements (E, inset). In turn, the high-grade component showed faint decoration for cytokeratin with paranuclear dot-like quality (F) and chromogranin A (G), while Ki-67 labeling index turned out to be very high (about 60%) (H). No differences were instead observed for synaptophysin labeling between the two cell components (D and G, insets). IHC, immunohistochemistry.

This implies that histologically poorly differentiated neoplasms amenable of complete resection and running a more favorable clinical course could harbor these evolving secondary high-grade NE tumors. It will be essential to clarify if these tumors correspond to progressing lesions, which are in turn highlighted by heterogenous Ki-67 LI, in

order to understand their pathological basis and explore the most appropriate clinical management.

Conclusions

Our understanding of Lu-NET is rapidly expanding,

especially regarding diagnosis, IHC marker choice and pathogenetic mechanisms, although adapting the morphology-based classification to the personalized and precision medicine is still challenging. This holds true in NETs of other organs as well. The assumption of differential genomic alterations between well-differentiated NE tumors and high-grade NE carcinomas of the lung and thymus is substantiated by multiple studies, but reassembling the existing data under the concept of secondary high-grade NETs has led to a possible paradigm shift in the pathogenesis of NETs.

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Footnote

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